

# Exhibit A



## Protein

PubMed Nucleotide Protein Genome Structure PopSet Taxonomy OMIM

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□ 1: P75966

LOCUS YMFC\_ECOLI 207 aa BCT 15-JUL-1998  
 DEFINITION HYPOTHETICAL 23.7 KD PROTEIN IN TRMU-ICDA INTERGENIC REGION.  
 ACCESSION P75966  
 PID g2501525  
 VERSION P75966 GI:2501525  
 DBSOURCE swissprot: locus YMFC\_ECOLI, accession P75966;  
 class: standard.  
 created: Nov 1, 1997.  
 sequence updated: Nov 1, 1997.  
 annotation updated: Jul 15, 1998.  
 xrefs: gi: gi: 1787371, gi: gi: 1787380  
 xrefs (non-sequence databases): ECOGENE EG13447, PROSITE PS01149  
 KEYWORDS HYPOTHETICAL PROTEIN.  
 SOURCE Escherichia coli.  
 ORGANISM Escherichia coli  
 Eubacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
 Escherichia.  
 REFERENCE 1 (residues 1 to 207)  
 AUTHORS BLATTNER, F.R., PLUNKETT, G.I.I.I., MAYHEW, G.F., PERNA, N.T. and  
 GLASNER, F.D.  
 TITLE Direct Submission  
 JOURNAL Submitted (??-JAN-1997) TO EMBL/GENBANK/DDBJ DATA BANKS  
 REMARK SEQUENCE FROM N.A.  
 STRAIN=K12 / MG1655  
 COMMENT [WARNING] On Nov 23, 1998 this sequence was replaced by a newer  
 version gi:3916025.  
 [SIMILARITY] STRONG, TO H.INFLUENZAE HI0694.  
 [SIMILARITY] BELONGS TO THE RSUA FAMILY OF PSEUDOURIDINE SYNTHASE.  
 FEATURES Location/Qualifiers  
 source 1..207  
 /organism="Escherichia coli"  
 /db\_xref="taxon:562"  
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 Protein 1..207  
 /product="HYPOTHETICAL 23.7 KD PROTEIN IN TRMU-ICDA  
 INTERGENIC REGION"  
 ORIGIN  
 1 mqktsfrnhq vkrfssqrst rrkpenqptr wilfnkpydv lpqftdeagr ktlkefipvq  
 61 gvyaaqrldr dsegllvltn ngalqarltq pgkrtgkiyy vqvegipqtd alealrngvt  
 121 lndgptlpag aelvdepawl wprnppirer ksiptswlki tlyegrnrqv rrmtnahvgfp  
 181 tlrlirvamq dvslndnlang ewrevtd

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